

IN THE CLAIMS

Please amend claims 1, 6, 27, and 29 and cancel claims 3-5, 8-26, and 33-38 without any prejudice or disclaimer to the subject matter expressed therein as indicated in the complete listing of all claims in the application set forth below.

Claim 1. (Amended) An isolated DNA sequence up to 20 kb in length comprising a nucleic acid sequence ~~as shown in SEQ ID NO. 1 that is SEQ ID NO: 1.~~

Claim 2. (Original) The isolated nucleic acid of claim 1, wherein said nucleic acid is cDNA.

Claims 3-5. (Canceled)

Claim 6. (Currently Amended) An oligonucleotide of at least 8 consecutive nucleotides selected from a sequence unique to ~~SEQ ID NO. 1~~ SEQ ID NO: 1 or the complement of ~~SEQ ID NO. 1~~ SEQ ID NO: 1, wherein said oligonucleotide has a single nucleotide substitution of A-to-C at position 734 (A734C) in exon 5 of said SEQ ID NO: 1 in comparison with non-mutated SLC11A3.

Claim 7. (Original) The oligonucleotide of claim 6, wherein the oligonucleotide is a member of an oligonucleotide pair for amplification of an HH nucleic acid sequence.

Claims 8-26. (Canceled)

Claim 27. (Currently Amended) A kit for the detection of the presence or absence of a an A-to-C base mutation at position 734 (A734C) of the SLC11A3 gene comprising an antibody which specifically binds to a gene product of the mutated SLC11A3 gene in combination with a reagent for detecting binding of the antibody to the gene product.

Claim 28. (Original) The kit of claim 27, further comprising primers for amplifying the DNA containing the base-pair polymorphism at position 734 (A734C) of the SLC11A3 gene.

Claim 29. (Currently Amended) A genetic marker predictive of a hereditary hemochromatosis (HH) gene mutation comprising a partial sequence of ~~SEQ ID NO. 1~~ SEQ ID NO: 1 having a single nucleotide substitution of A-to-C at position 734 (A734C) in exon 5 in comparison with non-mutated SLC11A3 and sequences complementary therewith.

Claim 30. (Previously Presented) A method for diagnosing a patient as having an increased risk of developing HH disease, comprising:

providing the isolated DNA sequence of claim 1 from the individual; and

assessing the isolated DNA sequence for the presence or absence of a base mutation at position 734 (A734C) of the SLC11A3

gene, wherein the absence of the base mutation indicates the absence of a HH gene mutation in the genome of the individual and the presence of the base mutation indicates the presence of the HH gene mutation and an increased risk of developing HH disease in the genome of the individual being diagnosed.

Claim 31. (Previously Presented) The method of claim 30, wherein the assessing step is performed by a process which comprises subjecting the isolated DNA sequence to amplification using oligonucleotide primers flanking the base-pair mutation.

Claim 32. (Previously Presented) The method of claim 31, wherein the assessing step further comprises an oligonucleotide ligation assay.

Claims 33-38. (Canceled)